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<p>(21) International Application Number: PCT/DK93/00003</p> <p>(22) International Filing Date: 7 January 1993 (07.01.93)</p> <p>(30) Priority data: PCT/DK92/00004 7 January 1992 (07.01.92) WO (34) Countries for which the regional or international application was filed: AT et al.</p> <p>(71) Applicant (for all designated States except US): NOVO NORDISK A/S [DK/DK]; Novo Allé, DK-2880 Bagsværd (DK).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): NORRIS, Fanny [DK/DK]; NORRIS, Kjeld [DK/DK]; Ahlmanns Allé 34, DK-2900 Hellerup (DK). BJØRN, Søren, Erik [DK/DK]; Marie Grubbes Allé 47, DK-2800 Lyngby (DK). PETERSEN, Lars, Christian [DK/DK]; Havevej 4, DK-2970 Hørsholm (DK). OLSEN, Ole, Hvilsted [DK/DK]; Bækkeskovvej 38, DK-2700 Brønshøj (DK).</p>	<p>(74) Common Representative: NOVO NORDISK A/S; Novo Allé, DK-2880 Bagsværd (DK).</p> <p>(81) Designated States: AU, CA, CZ, FI, HU, JP, KR, NO, NZ, PL, RU, SK, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p>Published With international search report.</p>	
<p>(54) Title: A HUMAN KUNITZ-TYPE PROTEASE INHIBITOR VARIANT</p> <p style="text-align: center;">F W C L</p> <p>X<sup>1</sup> Ser Trp Cys Leu Thr Pro Ala Asp X<sup>2</sup> Gly X<sup>3</sup> Cys X<sup>4</sup> X<sup>5</sup> X<sup>6</sup> X<sup>7</sup> X<sup>8</sup> X<sup>9</sup> Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe X<sup>10</sup> Tyr X<sup>11</sup> Gly Cys X<sup>12</sup> X<sup>13</sup> X<sup>14</sup> Glu Asn Asn Phe X<sup>15</sup> Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys X<sup>16</sup></p> <p style="text-align: right;">(I)</p> <p style="text-align: right;">M07K 201:00 M07K 207:00</p>		
<p>(57) Abstract</p> <p>A variant of human Kunitz-type protease inhibitor domain III of tissue factor protease inhibitor (TFPI), the variant comprising the amino acid sequence (I) wherein X<sup>1</sup> represents H or 1-5 naturally occurring amino acid residues except Cys, X<sup>2</sup>-X<sup>15</sup> each independently represents a naturally occurring amino acid residue, and X<sup>16</sup> represents OH or 1-5 naturally occurring amino acid residues except Cys, with the proviso that at least one of the amino acid residues X<sup>1</sup>-X<sup>16</sup> is different from the corresponding amino acid residue of the native sequence.</p>		

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## A HUMAN KUNITZ-TYPE PROTEASE INHIBITOR VARIANT

## FIELD OF INVENTION

5 The present invention relates to a variant of a human Kunitz-type protease inhibitor domain, DNA encoding the variant, a method of producing the variant and a pharmaceutical composition containing the variant.

## 10 BACKGROUND OF THE INVENTION

Polymorphonuclear leukocytes (neutrophils or PMNs) and mononuclear phagocytes (monocytes) play an important part in tissue injury, infection, acute and chronic inflammation and wound healing. The cells migrate from the blood to the site of inflammation and, following appropriate stimulation, they release oxidant compounds ( $O_2^*$ ,  $O_2^-$ ,  $H_2O_2$  and  $HOCl$ ) as well as granules containing a variety of proteolytic enzymes. The secretory granules contain, i.a., alkaline phosphatase, metalloproteinases such as gelatinase and collagenase and serine proteases such as neutrophil elastase, cathepsin G and proteinase 3.

Latent metalloproteinases are released together with tissue inhibitor of metalloproteinase (TIMP). The activation mechanism has not been fully elucidated, but it is likely that oxidation of thiol groups and/or proteolysis play a part in the process. Also, free metalloproteinase activity is dependent on inactivation of TIMP.

30

In the azurophil granules of the leukocytes, the serine proteases neutrophil elastase, cathepsin G and proteinase-3 are packed as active enzymes complexed with glucosaminoglycans. These complexes are inactive but dissociate on secretion to release the active enzymes. To neutralise the protease activity, large amounts of the inhibitors  $\alpha_1$ -proteinase inhibitor ( $\alpha_1$ -PI) and  $\alpha_1$ -chymotrypsin inhibitor ( $\alpha_1$ -ChI) are found in plasma. However, the PMNs are able to inactivate the inhibitors locally.

Thus,  $\alpha_1$ -PI which is the most important inhibitor of neutrophil elastase is sensitive to oxidation at the reactive centre (Met-358) by oxygen metabolites produced by triggered PMNs. This reduces the affinity of  $\alpha_1$ -PI for neutrophil elastase by approximately 2000 times.

After local neutralisation of  $\alpha_1$ -PI, the elastase is able to degrade a number of inhibitors of other proteolytic enzymes. Elastase cleaves  $\alpha_1$ -ChI and thereby promotes cathepsin G activity. It also cleaves TIMP, resulting in tissue degradation by metalloproteinases. Furthermore, elastase cleaves antithrombin III and heparin cofactor II, and tissue factor pathway inhibitor (TFPI) which probably promotes clot formation. On the other hand, the ability of neutrophil elastase to degrade coagulation factors is assumed to have the opposite effect so that the total effect of elastase is unclear. The effect of neutrophil elastase on fibrinolysis is less ambiguous. Fibrinolytic activity increases when the elastase cleaves the plasminogen activator inhibitor and the  $\alpha_2$  plasmin inhibitor. Besides, both of these inhibitors are oxidated and inactivated by  $O_2$  metabolites.

PMNs contain large quantities of serine proteases, and about 200 mg of each of the leukocyte proteases are released daily to deal with invasive agents in the body. Acute inflammation leads to a many-fold increase in the amount of enzyme released. Under normal conditions, proteolysis is kept at an acceptably low level by large amounts of the inhibitors  $\alpha_1$ -PI,  $\alpha_1$ -ChI and  $\alpha_2$  macroglobulin. There is some indication, however, that a number of chronic diseases is caused by pathological proteolysis due to overstimulation of the PMNs, for instance caused by autoimmune response, chronic infection, tobacco smoke or other irritants, etc.

Aprotinin (bovine pancreatic trypsin inhibitor) is known to inhibit various serine proteases, including trypsin, chymotrypsin, plasmin and kallikrein, and is used

therapeutically in the treatment of acute pancreatitis, various states of shock syndrome, hyperfibrinolytic haemorrhage and myocardial infarction (cf., for instance, J.E. Trapnell et al, Brit. J. Surg. 61, 1974, p. 177; J. McMichan et al., Circulatory shock 9, 1982, p. 107; L.M. Auer et al., Acta Neurochir. 49, 1979, p. 207; G. Sher, Am. J. Obstet. Gynecol. 129, 1977, p. 164; and B. Schneider, Artzneim.-Forsch. 26, 1976, p. 1606). Administration of aprotinin in high doses significantly reduces blood loss in connection with cardiac surgery, including cardiopulmonary bypass operations (cf., for instance, B.P. Bidstrup et al., J. Thorac. Cardiovasc. Surg. 97, 1989, pp. 364-372; W. van Oeveren et al., Ann. Thorac. Surg. 44, 1987, pp. 640-645). It has previously been demonstrated (cf. H.R. Wenzel and H. Tschesche, Angew. Chem. Internat. Ed. 20, 1981, p. 295) that certain aprotinin analogues, e.g. aprotinin(1-58, Val15) exhibits a relatively high selectivity for granulocyte elastase and an inhibitory effect on collagenase, aprotinin (1-58, Ala15) has a weak effect on elastase, while aprotinin (3-58, Arg15, Ala17, Ser42) exhibits an excellent plasma kallikrein inhibitory effect (cf. WO 89/10374).

However, when administered in vivo, aprotinin has been found to have a nephrotoxic effect in rats, rabbits and dogs after repeated injections of relatively high doses of aprotinin (Bayer, Trasylol, Inhibitor of proteinase; E. Glaser et al. in "Verhandlungen der Deutschen Gesellschaft für Innere Medizin, 78. Kongress", Bergmann, München, 1972, pp. 1612-1614). The nephrotoxicity (i.a. appearing in the form of lesions) observed for aprotinin might be ascribed to the accumulation of aprotinin in the proximal tubulus cells of the kidneys as a result of the high positive net charge of aprotinin which causes it to be bound to the negatively charged surfaces of the tubuli.. This nephrotoxicity makes aprotinin less suitable for clinical purposes, in particular those requiring administration of large doses of the inhibitor (such as cardiopulmonary bypass operations). Besides, aprotinin is a bovine protein which may therefore contain one or more epitopes which may give rise to an

undesirable immune response on administration of aprotinin to humans.

It is therefore an object of the present invention to identify human protease inhibitors of the same type as aprotinin (i.e. Kunitz-type inhibitors) with a similar inhibitor profile or modified to exhibit a desired inhibitor profile.

#### SUMMARY OF THE INVENTION

10

The present invention relates to a variant of human Kunitz-type protease inhibitor domain III of tissue factor pathway inhibitor (TFPI), the variant comprising the following amino acid sequence

15 X<sup>1</sup> Ser Trp Cys Leu Thr Pro Ala Asp X<sup>2</sup> Gly X<sup>3</sup> Cys X<sup>4</sup> X<sup>5</sup> X<sup>6</sup> X<sup>7</sup> X<sup>8</sup> X<sup>9</sup>  
Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe X<sup>10</sup> Tyr X<sup>11</sup>  
Gly Cys X<sup>12</sup> X<sup>13</sup> X<sup>14</sup> Glu Asn Asn Phe X<sup>15</sup> Ser Lys Gln Glu Cys Leu Arg  
Ala Cys Lys Lys X<sup>16</sup> (SEQ ID No. 1)

20 wherein X<sup>1</sup> represents H or 1-5 naturally occurring amino acid residues except Cys, X<sup>2</sup>-X<sup>15</sup> each independently represents a naturally occurring amino acid residue except Cys, and X<sup>16</sup> represents OH or 1-5 naturally occurring amino acid residues except Cys, with the proviso that at least one of the amino acid  
25 residues X<sup>1</sup>-X<sup>16</sup> is different from the corresponding amino acid residue of the native sequence.

In the present context, the term "naturally occurring amino acid residue" is intended to indicate any one of the 20 commonly  
30 occurring amino acids, i.e. Ala, Val, Leu, Ile Pro, Phe, Trp, Met, Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, Glu, Lys, Arg and His.

TFPI, also known as extrinsic pathway inhibitor (EPI) or  
35 lipoprotein associated coagulation inhibitor (LACI), has been isolated by Broze et al. (Proc. Natl. Acad. Sci. USA 84, 1987, pp. 1886-1890 and EP 300 988) and the gene coding for the

protein has been cloned, cf. EP 318 451. Analysis of the secondary structure of the protein has shown that the protein has three Kunitz-type inhibitor domains, from amino acid 22 to amino acid 79 (I), from amino acid 93 to amino acid 150 (II) and from amino acid 185 to amino acid 242 (III). Kunitz-type domain I of TFPI has been shown to bind TF/FVIIa, while Kunitz-type domain II has been shown to bind to FXa (Girard et al., Nature 338, 1989, pp. 518-520).

10 By substituting one or more amino acids in one or more of the positions indicated above, it may be possible to change the inhibitor profile of TFPI Kunitz-type domain III so that it preferentially inhibits neutrophil elastase, cathepsin G and/or proteinase-3. Furthermore, it may be possible to construct  
15 variants which specifically inhibit enzymes involved in coagulation or fibrinolysis (e.g. plasmin or plasma kallikrein) or the complement cascade.

One advantage of TFPI Kunitz-type domain III is that it has a  
20 negative net charge as opposed to aprotinin which, as indicated above, has a strongly positive net charge. It is therefore possible to construct variants of the invention with a lower positive net charge than aprotinin, thereby reducing the risk of kidney damage on administration of large doses of the variants.  
25 Another advantage is that, contrary to aprotinin, it is a human protein (fragment) so that undesired immunological reactions on administration to humans are significantly reduced.

#### DETAILED DISCLOSURE OF THE INVENTION

30 Examples of preferred variants of Kunitz-type domain III of TFPI are variants wherein X<sup>1</sup> is Gly-Pro; or wherein X<sup>2</sup> is an amino acid residue selected from the group consisting of Ala, Arg, Thr, Asp, Pro, Glu, Lys, Gln, Ser, Ile and Val, in particular  
35 wherein X<sup>2</sup> is Thr or Arg; or wherein X<sup>3</sup> is an amino acid residue selected from the group consisting of Pro, Thr, Leu, Arg, Val and Ile, in particular wherein X<sup>3</sup> is Pro or Leu; or wherein X<sup>4</sup> is

an amino acid residue selected from the group consisting of Lys, Arg, Val, Thr, Ile, Leu, Phe, Gly, Ser, Met, Trp, Tyr, Gln, Asn and Ala, in particular wherein  $X^4$  is Lys, Val, Leu, Ile, Thr, Met, Gln or Arg; or wherein  $X^5$  is an amino acid residue selected from the group consisting of Ala, Gly, Thr, Arg, Phe, Gln and Asp, in particular wherein  $X^5$  is Ala, Thr, Asp or Gly; or wherein  $X^6$  is an amino acid residue selected from the group consisting of Arg, Ala, Lys, Leu, Gly, His, Ser, Asp, Gln, Glu, Val, Thr, Tyr, Phe, Asn, Ile and Met, in particular wherein  $X^6$  is Arg, Phe, Ala, Asn, Leu or Tyr; or wherein  $X^7$  is an amino acid residue selected from the group consisting of Ile, Met, Gln, Glu, Thr, Leu, Val and Phe, in particular wherein  $X^7$  is Ile or Glu; or wherein  $X^8$  is an amino acid residue selected from the group consisting of Ile, Thr, Leu, Asn, Lys, Ser, Gln, Glu, Arg, Pro and Phe, in particular wherein  $X^8$  is Ile or Asn; or wherein  $X^9$  is an amino acid residue selected from the group consisting of Arg, Ser, Ala, Gln, Lys and Leu, in particular wherein  $X^9$  is Arg; or wherein  $X^{10}$  is an amino acid residue selected from the group consisting of Gln, Pro, Phe, Ile, Lys, Trp, Ala, Thr, Leu, Ser, Tyr, His, Asp, Met, Arg and Val, in particular wherein  $X^{10}$  is Val or Lys; or wherein  $X^{11}$  is Ser or Gly; or wherein  $X^{12}$  is an amino acid residue selected from the group consisting of Gly, Met, Gln, Glu, Leu, Arg, Lys, Pro and Asn, in particular wherein  $X^{12}$  is Arg or Glu; or wherein  $X^{13}$  is Ala or Gly; or wherein  $X^{14}$  is an amino acid residue selected from the group consisting of Lys, Asn and Asp, in particular wherein  $X^{14}$  is Lys or Asn; or wherein  $X^{15}$  is an amino acid residue selected from the group consisting of Val, Tyr, Asp, Glu, Thr, Gly, Leu, Ser, Ile, Gln, His, Asn, Pro, Phe, Met, Ala, Arg, Trp and Lys, in particular wherein  $X^{15}$  is Lys or Thr; or wherein  $X^{16}$  is Gly. In a preferred embodiment,  $X^1$  is Lys-Pro and  $X^{16}$  is Gly, while  $X^2$ - $X^{15}$  are as defined above.

Variants of TFPI Kunitz-type domain III of the invention should preferably not contain a Met residue in the protease binding region (i.e. the amino acid residues represented by  $X^3$ - $X^{14}$ ). By analogy to  $\alpha 1$ -PI described above, a Met residue in any one of these positions would make the inhibitor sensitive to oxidative



inactivation by oxygen metabolites produced by PMNs, and conversely, lack of a Met residue in these positions should render the inhibitor more stable in the presence of such oxygen metabolites.

5

A currently preferred variant of the invention is one in which one or more of the amino acid residues located at the protease-binding site of the Kunitz domain (i.e. one or more of X<sup>3</sup>-X<sup>14</sup> corresponding to positions 13, 15, 16, 17, 18, 19, 20, 34, 39, 10 40, 41 and 46 of aprotinin) are substituted to the amino acids present in the same positions of native aprotinin. This variant comprises the following amino acid sequence

Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Pro Cys Lys Ala  
15 Arg Ile Ile Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro  
Phe Val Tyr Gly Gly Cys Arg Ala Lys Glu Asn Asn Phe Lys Ser Lys  
Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly (SEQ ID No. 2).

In another aspect, the invention relates to a DNA construct  
20 encoding a human Kunitz-type inhibitor domain variant according to the invention. The DNA construct of the invention may be prepared synthetically by established standard methods, e.g. the phosphoramidite method described by S.L. Beaucage and M.H. Caruthers, Tetrahedron Letters 22, 1981, pp. 1859-1869, or the  
25 method described by Matthes et al., EMBO Journal 3, 1984, pp. 801-805. According to the phosphoramidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in suitable  
vectors.

30

Alternatively, it is possible to use genomic or cDNA coding for  
TFPI Kunitz-type domain III (e.g. obtained by screening a  
genomic or cDNA library for DNA coding for TFPI using synthetic  
oligonucleotide probes and isolating the DNA sequence coding for  
35 domain III therefrom). The DNA sequence is modified at one or more sites corresponding to the site(s) at which it is desired to introduce amino acid substitutions, e.g. by site-directed

mutagenesis using synthetic oligonucleotides encoding the desired amino acid sequence for homologous recombination in accordance with well-known procedures.

5 In a still further aspect, the invention relates to a recombinant expression vector which comprises a DNA construct of the invention. The recombinant expression vector may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the  
10 host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into  
15 a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence encoding the TFPI Kunitz-type  
20 domain III variant of the invention should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of  
25 suitable promoters for directing the transcription of the DNA encoding the TFPI Kunitz-type domain III variant of the invention in mammalian cells are the SV 40 promoter (Subramani et al., Mol. Cell Biol. 1, 1981, pp. 854-864), the MT-1 (metallothionein gene) promoter (Palmiter et al., Science 222,  
30 1983, pp. 809-814) or the adenovirus 2 major late promoter. Suitable promoters for use in yeast host cells include promoters from yeast glycolytic genes (Hitzeman et al., J. Biol. Chem. 255, 1980, pp. 12073-12080; Alber and Kawasaki, J. Mol. Appl. Gen. 1, 1982, pp. 419-434) or alcohol dehydrogenase genes (Young et al., in Genetic Engineering of Microorganisms for Chemicals  
35 (Hollaender et al, eds.), Plenum Press, New York, 1982), or the TPI1 (US 4, 599, 311) or ADH2-4c (Russell et al., Nature 304,

1983, pp. 652-654) promoters. Suitable promoters for use in filamentous fungus host cells are, for instance, the ADH3 promoter (McKnight et al., The EMBO J. 4, 1985, pp. 2093-2099) or the tpiA promoter.

5

The DNA sequence encoding the TFPI Kunitz-type domain III variant of the invention may also be operably connected to a suitable terminator, such as the human growth hormone terminator (Palmiter et al., op. cit.) or (for fungal hosts) the TPI1  
10 (Alber and Kawasaki, op. cit.) or ADH3 (McKnight et al., op. cit.) promoters. The vector may further comprise elements such as polyadenylation signals (e.g. from SV 40 or the adenovirus 5 Elb region), transcriptional enhancer sequences (e.g. the SV 40 enhancer) and translational enhancer sequences (e.g. the ones  
15 encoding adenovirus VA RNAs).

The recombinant expression vector of the invention may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. An examples of such a sequence (when the  
20 host cell is a mammalian cell) is the SV 40 origin of replication, or (when the host cell is a yeast cell) the yeast plasmid 2 $\mu$  replication genes REP 1-3 and origin of replication. The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such  
25 as the gene coding for dihydrofolate reductase (DHFR) or one which confers resistance to a drug, e.g. neomycin, hygromycin or methotrexate, or the Schizosaccharomyces pombe TPI gene (described by P.R. Russell, Gene 40, 1985, pp. 125-130).

30 The procedures used to ligate the DNA sequences coding for the TFPI Kunitz-type domain III variant of the invention, the promoter and the terminator, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf.,  
35 for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989).

The host cell into which the expression vector of the invention is introduced may be any cell which is capable of producing the TFPI Kunitz-type domain III variant of the invention and is preferably a eukaryotic cell, such as a mammalian, yeast or  
5 fungal cell.

The yeast organism used as the host cell according to the invention may be any yeast organism which, on cultivation, produces large quantities of the TFPI Kunitz-type domain III  
10 variant of the invention. Examples of suitable yeast organisms are strains of the yeast species Saccharomyces cerevisiae, Saccharomyces kluyveri, Schizosaccharomyces pombe or Saccharomyces uvarum. The transformation of yeast cells may for instance be effected by protoplast formation followed by  
15 transformation in a manner known per se.

Examples of suitable mammalian cell lines are the COS (ATCC CRL 1650), BHK (ATCC CRL 1632, ATCC CCL 10) or CHO (ATCC CCL 61) cell lines. Methods of transfecting mammalian cells and  
20 expressing DNA sequences introduced in the cells are described in e.g. Kaufman and Sharp, J. Mol. Biol. 159, 1982, pp. 601-621; Southern and Berg, J. Mol. Appl. Genet. 1, 1982, pp. 327-341; Loyter et al., Proc. Natl. Acad. Sci. USA 79, 1982, pp. 422-426; Wigler et al., Cell 14, 1978, p. 725; Corsaro and Pearson,  
25 Somatic Cell Genetics 7, 1981, p. 603, Graham and van der Eb, Virology 52, 1973, p. 456; and Neumann et al., EMBO J. 1, 1982, pp. 841-845.

Alternatively, fungal cells may be used as host cells of the  
30 invention. Examples of suitable fungal cells are cells of filamentous fungi, e.g. Aspergillus spp. or Neurospora spp., in particular strains of Aspergillus oryzae or Aspergillus niger. The use of Aspergillus spp. for the expression of proteins is described in, e.g., EP 238 023.

35

The present invention further relates to a method of producing a TFPI Kunitz-type domain III variant according to the

invention, the method comprising culturing a cell as described above under conditions conducive to the expression of the variant and recovering the resulting variant from the culture.

5 The medium used to cultivate the cells may be any conventional medium suitable for growing mammalian cells or fungal (including yeast) cells, depending on the choice of host cell. The variant will be secreted by the host cells to the growth medium and may be recovered therefrom by conventional procedures including  
10 separating the cells from the medium by centrifugation or filtration, precipitating the proteinaceous components of the supernatant or filtrate by means of a salt, e.g. ammonium sulfate, purification by a variety of chromatographic procedures, e.g. ion exchange chromatography or affinity  
15 chromatography, or the like.

The present invention also relates to a pharmaceutical composition comprising a TFPI Kunitz-type domain III variant of the invention together with a pharmaceutically acceptable  
20 carrier or excipient. In the composition of the invention, the variant may be formulated by any of the established methods of formulating pharmaceutical compositions, e.g. as described in Remington's Pharmaceutical Sciences, 1985. The composition may typically be in a form suited for systemic injection or infusion  
25 and may, as such, be formulated with sterile water or an isotonic saline or glucose solution.

The TFPI Kunitz-type domain III variant of the invention is therefore contemplated to be advantageous to use for the  
30 therapeutic applications suggested for native aprotinin or aprotinin analogues with other inhibitor profiles, in particular those which necessitate the use of large aprotinin doses. Therapeutic applications for which the use of the variant of the invention is indicated as a result of its ability to inhibit  
35 human serine proteases, e.g. trypsin, plasmin, kallikrein, elastase, cathepsin G and proteinase-3, include (but are not limited to) acute pancreatitis, inflammation, thrombocytopenia,

preservation of platelet function, organ preservation, wound healing, shock (including shock lung) and conditions involving hyperfibrinolytic haemorrhage, emphysema, rheumatoid arthritis, adult respiratory distress syndrome, chronic inflammatory bowel  
5 disease and psoriasis, in other words diseases presumed to be caused by pathological proteolysis by elastase, cathepsin G and proteinase-3 released from triggered PMNs.

Furthermore, the present invention relates to the use of TFPI  
10 Kunitz-type inhibitor domain III or a variant thereof as described above for the preparation of a medicament for the prevention or therapy of diseases or conditions associated with pathological proteolysis by proteases released from  
overstimulated PMNs. As indicated above, it may be an advantage  
15 of administer heparin concurrently with the TFPI Kunitz-type inhibitor domain III or variant.

Apart from the pharmaceutical use indicated above, TFPI Kunitz-type domain II or a variant thereof as specified above may be  
20 used to isolate useful natural substances, e.g. proteases or receptors from human material, which bind directly or indirectly to TFPI Kunitz-type domain II, for instance by screening assays or by affinity chromatography.

(A) NAME: Novo Nordisk A/S  
(B) STREET: Novo Alle  
(C) CITY: Bagsvaerd  
(E) COUNTRY: Denmark  
(F) POSTAL CODE (ZIP): DK-2880  
(G) TELEPHONE: +45 4444 8888  
(H) TELEFAX: +45 4449 3256  
(I) TELEX: 37304

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) ORGANISM: synthetic

Xaa Ser Trp Cys Leu Thr Pro Ala Asp Xaa Gly Xaa Cys Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe  
20 25 30

Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Glu Asn Asn Phe Xaa Ser Lys Gln  
35 40 45

Glu Cys Leu Arg Ala Cys Lys Lys Xaa  
50 55

(2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: synthetic

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Pro Cys Lys Ala  
1 5 10 15

Arg Ile Ile Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro  
20 25 30

Phe Val Tyr Gly Gly Cys Gly Arg Lys Glu Asn Asn Phe Lys Ser Lys  
35 40 45

Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly  
50 55



## CLAIMS

1. A variant of human Kunitz-type protease inhibitor domain III  
 5 of tissue factor protease inhibitor (TFPI), the variant  
 comprising the following amino acid sequence

<sup>3</sup> <sup>4</sup> <sup>10</sup> <sup>90</sup>  
 X<sup>1</sup> Ser Trp Cys Leu Thr Pro Ala Asp X<sup>2</sup> Gly X<sup>3</sup> Cys X<sup>4</sup> X<sup>5</sup> X<sup>6</sup> X<sup>7</sup> X<sup>8</sup> X<sup>9</sup>  
 Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe X<sup>10</sup> Tyr X<sup>11</sup>  
 10 Gly Cys X<sup>12</sup> X<sup>13</sup> X<sup>14</sup> Glu Asn Asn Phe X<sup>15</sup> Ser Lys Gln Glu Cys Leu Arg  
 Ala Cys Lys Lys X<sup>16</sup> (SEQ ID No. 1)

wherein X<sup>1</sup> represents H or 1-5 naturally occurring amino acid  
 residues except Cys, X<sup>2</sup>-X<sup>15</sup> each independently represents a  
 15 naturally occurring amino acid residue, and X<sup>16</sup> represents OH or  
 1-5 naturally occurring amino acid residues except Cys, with the  
 proviso that at least one of the amino acid residues X<sup>1</sup>-X<sup>16</sup> is  
 different from the corresponding amino acid residue of the  
 native sequence.

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2. A variant according to claim 1, wherein X<sup>1</sup> is Gly-Pro.

3. A variant according to claim 1, wherein X<sup>2</sup> is an amino acid  
 residue selected from the group consisting of Ala, Arg, Thr,  
 25 Asp, Pro, Glu, Lys, Gln, Ser, Ile and Val.

4. A variant according to claim 3, wherein X<sup>2</sup> is Thr or Arg.

5. A variant according to claim 1, wherein X<sup>3</sup> is an amino acid  
 30 residue selected from the group consisting of Pro, Thr, Leu,  
 Arg, Val and Ile.

6. A variant according to claim 5, wherein X<sup>3</sup> is Pro or Leu.

35 7. A variant according to claim 1, wherein X<sup>4</sup> is an amino acid  
 residue selected from the group consisting of Lys, Arg, Val,  
 Thr, Ile, Leu, Phe, Gly, Ser, Met, Trp, Tyr, Gln, Asn and Ala.

8. A variant according to claim 7, wherein X<sup>4</sup> is Lys, Val, Leu, Ile, Thr, Met, Gln or Arg.

6 9. A variant according to claim 1, wherein X<sup>5</sup> is an amino acid  
5 residue selected from the group consisting of Ala, Gly, Thr, Arg, Phe, Gln and Asp.

10. A variant according to claim 9, wherein X<sup>5</sup> is Ala, Thr, Asp or Gly.

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17 11. A variant according to claim 1, wherein X<sup>6</sup> is an amino acid  
residue selected from the group consisting of Arg, Ala, Lys, Leu, Gly, His, Ser, Asp, Gln, Glu, Val, Thr, Tyr, Phe, Asn, Ile and Met.

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12. A variant according to claim 11, wherein X<sup>6</sup> is Arg, Phe, Ala, Asn, Leu or Tyr.

18 13. A variant according to claim 1, wherein X<sup>7</sup> is an amino acid  
20 residue selected from the group consisting of Ile, Met, Gln, Glu, Thr, Leu, Val and Phe.

14. A variant according to claim 13, wherein X<sup>7</sup> is Ile or Glu.

25 15. A variant according to claim 1, wherein X<sup>8</sup> is an amino acid  
(9) residue selected from the group consisting of Ile, Thr, Leu, Asn, Lys, Ser, Gln, Glu, Arg, Pro and Phe.

16. A variant according to claim 15, wherein X<sup>8</sup> is Ile or Asn.

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20 17. A variant according to claim 1, wherein X<sup>9</sup> is an amino acid  
residue selected from the group consisting of Arg, Ser, Ala, Gln, Lys and Leu.

35 18. A variant according to claim 17, wherein X<sup>9</sup> is Arg.

34 19. A variant according to claim 1, wherein X<sup>10</sup> is an amino acid

residue selected from the group consisting of Gln, Pro, Phe, Ile Lys, Trp, Ala, Thr, Leu, Ser, Tyr, His, Asp, Met, Arg and Val.

20. A variant according to claim 19, wherein  $X^{10}$  is Val or Lys.

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21. A variant according to claim 1, wherein  $X^{11}$  is Ser or Gly. 36

22. A variant according to claim 1, wherein  $X^{12}$  is an amino acid residue selected from the group consisting of Gly, Met, Gln, Glu, Leu, Arg, Lys, Pro and Asn.

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23. A variant according to claim 22, wherein  $X^{12}$  is Ala or Leu. 39

24. A variant according to claim 1, wherein  $X^{13}$  is Ala or Gly.

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25. A variant according to claim 1, wherein  $X^{14}$  is an amino acid residue selected from the group consisting of Lys, Asn and Asp.

26. A variant according to claim 25, wherein  $X^{14}$  is Lys or Asn.

20

27. A variant according to claim 1, wherein  $X^{15}$  is an amino acid residue selected from the group consisting of Val, Tyr, Asp, Glu, Thr, Gly, Leu, Ser, Ile, Gln, His, Asn, Pro, Phe, Met, Ala, Arg, Trp and Lys.

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28. A variant according to claim 27, wherein  $X^{15}$  is Lys or Glu.

29. A variant according to claim 1, wherein  $X^{16}$  is Gly.

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30. A variant according to claim 1, wherein  $X^1$  is Gly-Pro and  $X^{16}$  is Gly.

31. A variant according to claim 1 comprising the following amino acid sequence

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Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Pro Cys Lys Ala  
Arg Ile Ile Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro

Phe Val Tyr Gly Gly Cys Gly Arg Lys Glu Asn Asn Phe Lys Ser Lys  
Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly (SEQ ID No. 2).

32. A DNA construct comprising a DNA sequence encoding a human  
5 Kunitz-type protease inhibitor variant according to any of  
claims 1-31.

33. A recombinant expression vector comprising a DNA construct  
according to claim 32.

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34. A cell containing a DNA construct according to claim 32 or  
an expression vector according to claim 33.

35. A method of producing a human Kunitz-type protease inhibitor  
15 variant according to any of claims 1-31, the method comprising  
culturing a cell according to claim 34 under conditions  
conducive to the expression of the protein, and recovering the  
resulting protein from the culture.

20 36. A pharmaceutical composition comprising a human Kunitz-type  
protease inhibitor variant according to any of claims 1-31 and  
a pharmaceutically acceptable carrier or excipient.

37. A composition according to claim 36 which further comprises  
25 heparin.

38. Use of human Kunitz-type protease inhibitor domain III of  
TFPI or a variant thereof according to any of claims 1-31 for  
the preparation of a medicament for the prevention or treatment  
30 of diseases or conditions associated with pathological  
proteolysis.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 93/00003

## A. CLASSIFICATION OF SUBJECT MATTER

IPC5: C07K 7/10, C12N 15/15, A61K 37/64

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC5: A61K, C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

## CHEMICAL ABSTRACTS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NATURE, Volume 338, April 1989, Thomas J. Girard et al, "Functional significance of the Kunitz-type inhibitory domains of lipoprotein-associated coagulation inhibitor"	1,7,8,35,36,38
A	--	2-6,9-34
A,P	US, A, 5106833 (BROZE, JR. ET AL), 21 April 1992 (21.04.92)	1-38
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☐ Further documents are listed in the continuation of Box C.☒ See patent family annex.

## \* Special categories of cited documents:

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"&amp;" document member of the same patent family

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Name and mailing address of the ISA/  
 Swedish Patent Office  
 Box 5055, S-102 42 STOCKHOLM  
 Facsimile No. +46 8 666 02 86

Authorized officer

Elisabeth Carlborg  
 Telephone No. +46 8 782 25 00

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